

Application of: Hoogenboom and Henderikx

Serial No.: **Continuation of U.S. Application  
09/538,913**

Filed: (concurrently herewith)

Entitled: MUCIN-1 SPECIFIC BINDING  
MEMBERS AND METHODS OF  
USE THEREOF

Attorney Docket No.: DYX-015.1 US

ART UNIT:

EXAMINER:

STATEMENT UNDER 37 C.F.R. § 1.821(f)

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

Applicants submit herewith a Sequence Listing in written and computer readable form under 37 C.F.R. § 1.821(a)-(e) complying with the provisions of 37 C.F.R. § 1.824. The sequence listing is being submitted along with the original application papers.

In accordance with 37 C.F.R. § 1.821(f), the undersigned attorney of record hereby states that the written form and the computer readable form of the Sequence Listing submitted herewith for the above-identified patent application are identical in content.

30-March-2001

Date



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## SEQUENCE LISTING

<110> DYAX CORP.  
 <120> MUCIN-1 Specific Binding Members and Methods of Use Thereof  
 <130> DYX-015.1 US, DYX-015.1 PCT  
 <140> not yet assigned  
 <141> 2001-03-30  
 <150> US 09/538,913  
 <151> 2000-03-30  
 <160> 112  
 <170> PatentIn version 3.0  
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Asn	Gly	Tyr	Thr	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	35	40	45	
Pro	Gln	Leu	Leu	Ile	Tyr	Ser	Gly	Ser	His	Arg	Ala	Ser	Gly	Val	Pro	50	55	60	
Asp	Arg	Phe	Ser	Gly	Ser	Val	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Arg	Ile	65	70	75	80
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Gly	85	90	95	
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 Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
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agc 363

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20 25 30  
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                     85                    90                    95

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly  
                     100                    105                    110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ala Leu Glu Ile  
                     115                    120                    125

Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro  
           130                    135                    140

Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly  
 145                    150                    155                    160

Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln  
                     165                    170                    175

Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro Asp Arg  
                     180                    185                    190

Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile Ser Arg  
           195                    200                    205

Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Leu Gln  
           210                    215                    220

Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Gly  
 225                    230                    235                    240

Gly Gly Ser Gly Gly Gly Ala Leu Ala Pro Thr Ser Ser Ser Thr Lys  
                     245                    250                    255

Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile  
           260                    265                    270

Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu  
           275                    280                    285

Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu  
           290                    295                    300

Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu  
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Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn

	325		330		335
Ile Asn Val	Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met				
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Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg					
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gttctggaac taaagggatc tgaaacaaca ttcattgtgtg aatatgctga tgagacagca      1080
accattgtag aattttctgaa cagatggatt accttttgtc aaagcatcat ctcaacactg      1140
act                                                                    1143

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<400> 8

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Pro Ala His Gly
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 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
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 85 90 95

Ala Lys

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 20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
 35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro  
 50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala  
 85 90 95

Leu Gln Thr Pro  
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42

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<400> 22

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 20 25 30

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 35 40 45

Pro Gln Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro  
 50 55 60

Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile  
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly  
85 90 95

Leu Gln Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys  
100 105 110

Arg Gly Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
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caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc      540
ctcagcagca ccttgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc      600
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20           25           30
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35           40           45
Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85           90           95
Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
100          105          110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115          120          125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130          135          140

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 165 170 175  
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 180 185 190  
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 195 200 205  
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 210 215 220  
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 225 230 235 240  
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 245 250 255  
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 260 265 270  
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 275 280 285  
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 290 295 300  
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 305 310 315 320  
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 325 330 335  
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 340 345 350  
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
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 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 370 375 380  
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

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1           5           10

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 1 5 10

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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
 1 5 10

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Ala Ile His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys Tyr  
 1 5 10

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 cccggtatgt ttgcacaat aatatacggc 90

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<400> 39  
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<400> 40

Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala Leu  
 1 5 10 15

<210> 41  
 <211> 16  
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<213> synthetic

<400> 41

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<210> 43

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<400> 43

Ala	Lys	Ser	Ser	Thr	Thr	Thr	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
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<400> 44

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48

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<221> PEPTIDE

<222> (1)..(16)

<223> Xaa is varied according to the disclosure

<400> 45

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 <222> (1)..(16)  
 <223> Xaa is varied according to the disclosure

<400> 47

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 1 5 10 15

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<400> 48  
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48

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<400> 49

Tyr Trp Gly  
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 <212> DNA  
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<400> 50  
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48

<210> 51  
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<400> 51

Ala Lys Arg Tyr Leu Tyr Asp Val Trp Asp Pro Ile Asp Tyr Trp Gly  
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<210> 52  
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<400> 52  
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48

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<400> 53

Ala Lys His Thr Gly Gly Gly Thr Leu Gln Arg Leu Asp Tyr Trp Gly  
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<210> 54  
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<400> 55

Ala	Lys	His	Thr	Gly	Gly	Gly	Thr	Gln	Thr	Pro	Cys	Asp	Tyr	Trp	Gly
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<400> 56

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48

<210> 57  
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<400> 57

Ala	Lys	His	Thr	Gly	Gly	Gly	Arg	Arg	Ile	Cys	His	Asp	Tyr	Trp	Gly
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48

<210> 59  
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<223> Xaa is varied according to the disclosure

<400> 59

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48

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<400> 61

Ala	Lys	His	Thr	Gly	Gly	Gly	Gln	Lys	Leu	Gln	Leu	Asp	Tyr	Trp	Gly
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<211> 48

<212> DNA

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<400> 62

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48

<210> 63

<211> 16

<212> PRT

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<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa may be varied according to the disclosure to form alternate peptide



&lt;400&gt; 63

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 1 5 10 15

&lt;210&gt; 64

&lt;211&gt; 48

&lt;212&gt; DNA

&lt;213&gt; synthetic

&lt;400&gt; 64

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&lt;210&gt; 65

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; synthetic

&lt;400&gt; 65

Ala Asn Gln Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly  
 1 5 10 15

&lt;210&gt; 66

&lt;211&gt; 48

&lt;212&gt; DNA

&lt;213&gt; synthetic

&lt;400&gt; 66

gcgaaccaga ctgggggggg cgtttgggac cccattgact actggggc 48

&lt;210&gt; 67

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; synthetic

&lt;400&gt; 67

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Tyr Tyr Trp Gly  
 1 5 10 15

&lt;210&gt; 68

&lt;211&gt; 48

&lt;212&gt; DNA

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<400> 68

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<211> 16

<212> PRT

<213> synthetic

<400> 69

Ala	Lys	Pro	Thr	Gly	Gly	Gly	Ala	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
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<400> 70

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<211> 16

<212> PRT

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<400> 71

Ala	Lys	His	Thr	Gly	Val	Gly	Val	Trp	His	Pro	Ile	Tyr	Tyr	Trp	Gly
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<211> 48

<212> DNA

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<400> 72

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48

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<400> 73

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<400> 74

Ala Lys His Thr Gly Glu Gly Val Trp Asp Pro Ile Lys Tyr  
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<210> 75

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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Lys  
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<400> 76

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
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Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
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<210> 78  
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<210> 82  
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1 5 10

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<400> 83

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr  
1 5 10

<210> 84  
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1 5 10

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<400> 86

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<210> 87  
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<400> 87

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<400> 88

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<400> 89

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Tyr  
1 5 10

<210> 90

<211> 14

<212> PRT

<213> synthetic

<400> 90

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Asn  
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<210> 91

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<212> PRT

<213> synthetic

<400> 91

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<210> 92

<211> 14  
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<400> 92

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 1 5 10

<210> 93  
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<400> 93

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met Asp Tyr  
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<400> 94

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 1 5 10

<210> 95  
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<210> 99  
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<400> 99

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<210> 100  
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<400> 101

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1 5 10

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<400> 103

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met His Tyr  
1 5 10

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<210> 105

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Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr  
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<210> 106

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 1 5 10

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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Tyr Tyr  
 1 5 10

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<400> 110

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tggtcccagg gcc 73

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<400> 112  
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